

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
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Application Serial Number: 10/579,025
Source: IFWP
Date Processed by STIC: 05/23/2006

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IFWP

RAW SEQUENCE LISTING

DATE: 05/23/2006

PATENT APPLICATION: US/10/579,025

TIME: 14:04:50

Input Set : A:\79535367.APP

Output Set: N:\CRF4\05232006\J579025.raw

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3 <110> APPLICANT: THERION BIOLOGICS CORPORATION
5 <120> TITLE OF INVENTION: CUSTOM VECTORS FOR TREATING AND PREVENTING PANCREATIC
6   CANCER
8 <130> FILE REFERENCE: 700953-53671-PCT
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/579,025
C--> 11 <141> CURRENT FILING DATE: 2006-05-11
13 <150> PRIOR APPLICATION NUMBER: 60/519,354
14 <151> PRIOR FILING DATE: 2003-11-12
16 <160> NUMBER OF SEQ ID NOS: 6
18 <170> SOFTWARE: PatentIn Ver. 3.3
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 1548
22 <212> TYPE: DNA
23 <213> ORGANISM: Homo sapiens
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27 gttacggggt ctggtcatgc aagctctacc ccaggtggag aaaaggagac ttcggctacc 120
28 cagagaagtt cagtgccag ctctactgag aagaatgctg tgagtatgac aagctccgta 180
29 ctctccagcc acagccccgg ttcaggctcc tccaccactc agggacagga tgtcactctg 240
30 gccccggcca cggaaccagc ttcaggttca gctgccttgt ggggacagga tgtcacctcg 300
31 gtaccagtta ctagaccagc tttaggttagc acagcacctc ctgctcatgg agtaactagt 360
32 gctcctgata ctctgccagc tcttggcagt actgcaccac cggcacatgg cgtaacatca 420
33 gcacctgata caagacctgc acctggatct acagcgccgc ctgcgcacgg agtgacatcg 480
34 gcgcccagata cgcgccccgc tcccggtagc accgcaccgc ccgcccacgg tgttacaagt 540
35 gcacccagata cccggccggc acccggaagt accgctccac ctgcacacgg ggtcacaagc 600
36 gcgcccagata ctgcacctgc gccagggtcg actgcccctc cggcgcatgg tgtgacctca 660
37 gctcctgata caaggccagc cccagctagc actctggtgc acaacggcac ctctgccagg 720
38 gctaccacaa cccagccag caagagcact ccattctcaa tcccagcca ccactctgat 780
39 actcctacca cccttgccag ccatagcacc aagactgatg ccagtagcac tcaccatagc 840
40 acggtacctc ctctcacctc ctccaatcac agcaattctc cccagttgtc tactggggtc 900
41 tctttctttt tctgtcttt tcaatttca aacctccagt ttaattctc tctggaagat 960
42 cccagcaccg actactacca agagctgcag agagacattt ctgaaatgtt tttgcagatt 1020
43 tataaacaag ggggttttct gggcctctcc aatattaagt tcaggccagg atctgtggtg 1080
44 gtacaattga ctctggcctt ccgagaaggt accatcaatg tccacgacgt ggagacacag 1140
45 ttcaatcagt ataaaacgga agcagcctct cgatataacc tgacgatctc agacgtcagc 1200
46 gtgagtgatg tgccatttcc tttctctgcc cagtctgggg ctgggggtgcc aggctggggc 1260
47 atcgcgctgc tgggtgctgg ctgtgttctg gttgcgctgg ccattgtcta tctcattgcc 1320
48 ttggtgtct gtcagtgcg ccgaaagaac tacgggcagc tggacatctt tccagcccg 1380
49 gatacctacc atcctatgag cgagtacccc acctaccaca cccatgggag ctatgtgccc 1440
50 cctagcagta ccgatcgtag cccctatgag aaggtttctg caggtaatgg tggcagcagc 1500
51 ctctcttaca caaacccagc agtggcagcc acttctgcca acttgtag 1548
54 <210> SEQ ID NO: 2
55 <211> LENGTH: 515

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56 <212> TYPE: PRT
57 <213> ORGANISM: Homo sapiens
58 <400> SEQUENCE: 2
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61   1           5           10           15
63 Val Leu Thr Val Val Thr Gly Ser Gly His Ala Ser Ser Thr Pro Gly
64           20           25           30
66 Gly Glu Lys Glu Thr Ser Ala Thr Gln Arg Ser Ser Val Pro Ser Ser
67           35           40           45
69 Thr Glu Lys Asn Ala Val Ser Met Thr Ser Ser Val Leu Ser Ser His
70           50           55           60
72 Ser Pro Gly Ser Gly Ser Ser Thr Thr Gln Gly Gln Asp Val Thr Leu
73   65           70           75           80
75 Ala Pro Ala Thr Glu Pro Ala Ser Gly Ser Ala Ala Leu Trp Gly Gln
76           85           90           95
78 Asp Val Thr Ser Val Pro Val Thr Arg Pro Ala Leu Gly Ser Thr Ala
79           100          105          110
81 Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro
82           115          120          125
84 Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala Pro Glu Thr
85           130          135          140
87 Arg Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser
88 145           150           155           160
90 Ala Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His
91           165           170           175
93 Gly Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala
94           180          185          190
96 Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro
97           195          200          205
99 Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr
100          210          215          220
102 Arg Pro Ala Pro Ala Ser Thr Leu Val His Asn Gly Thr Ser Ala Arg
103 225          230          235          240
105 Ala Thr Thr Thr Pro Ala Ser Lys Ser Thr Pro Phe Ser Ile Pro Ser
106           245          250          255
108 His His Ser Asp Thr Pro Thr Thr Leu Ala Ser His Ser Thr Lys Thr
109           260          265          270
111 Asp Ala Ser Ser Thr His His Ser Thr Val Pro Pro Leu Thr Ser Ser
112           275          280          285
114 Asn His Ser Thr Ser Pro Gln Leu Ser Thr Gly Val Ser Phe Phe Phe
115           290          295          300
117 Leu Ser Phe His Ile Ser Asn Leu Gln Phe Asn Ser Ser Leu Glu Asp
118 305           310          315          320
120 Pro Ser Thr Asp Tyr Tyr Gln Glu Leu Gln Arg Asp Ile Ser Glu Met
121           325          330          335
123 Phe Leu Gln Ile Tyr Lys Gln Gly Gly Phe Leu Gly Leu Ser Asn Ile
124           340          345          350
126 Lys Phe Arg Pro Gly Ser Val Val Gln Leu Thr Leu Ala Phe Arg
127           355          360          365

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129 Glu Gly Thr Ile Asn Val His Asp Val Glu Thr Gln Phe Asn Gln Tyr
130      370                      375                      380
132 Lys Thr Glu Ala Ala Ser Arg Tyr Asn Leu Thr Ile Ser Asp Val Ser
133 385                      390                      395                      400
135 Val Ser Asp Val Pro Phe Pro Phe Ser Ala Gln Ser Gly Ala Gly Val
136                      405                      410                      415
138 Pro Gly Trp Gly Ile Ala Leu Leu Val Leu Val Cys Val Leu Val Ala
139                      420                      425                      430
141 Leu Ala Ile Val Tyr Leu Ile Ala Leu Ala Val Cys Gln Cys Arg Arg
142                      435                      440                      445
144 Lys Asn Tyr Gly Gln Leu Asp Ile Phe Pro Ala Arg Asp Thr Tyr His
145 450                      455                      460
147 Pro Met Ser Glu Tyr Pro Thr Tyr His Thr His Gly Arg Tyr Val Pro
148 465                      470                      475                      480
150 Pro Ser Ser Thr Asp Arg Ser Pro Tyr Glu Lys Val Ser Ala Gly Asn
151                      485                      490                      495
153 Gly Gly Ser Ser Leu Ser Tyr Thr Asn Pro Ala Val Ala Ala Thr Ser
154                      500                      505                      510
156 Ala Asn Leu
157      515
160 <210> SEQ ID NO: 3
161 <211> LENGTH: 2106
162 <212> TYPE: DNA
163 <213> ORGANISM: Homo sapiens
165 <400> SEQUENCE: 3
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167 acagcctcac ttctaacctt ctggaacccg cccaccactg ccaagctcac tattgaatcc 120
168 acgccgttca atgtgcgaga ggggaaggag gtgctttctac ttgtccacaa tctgccccag 180
169 catctttttg gctacagctg gtacaaaggt gaaagagtgg atggcaaccg tcaaattata 240
170 ggatatgtaa taggaactca acaagctacc ccagggcccc catacagtgg tcgagagata 300
171 atatacccca atgcataccct gctgatccag aacatcatcc agaatgacac aggattctac 360
172 accctacacg tcataaagtc agatcttgtg aatgaagaag caactggcca gttccgggta 420
173 tacccggaac tccctaagcc ttctattagc tccaataata gtaagcctgt cgaagacaaa 480
174 gatgccgtcg cttttacatg cgagcccgaa actcaagacg caacatatct ctggtgggtg 540
175 aacaaccagt ccctgcctgt gtcccctaga ctccaactca gcaacggaaa tagaactctg 600
176 accctgttta acgtgaccag gaacgacaca gcaagctaca aatgcgaaac ccaaaatcca 660
177 gtcagcgcca ggaggtctga ttcagtgatt ctcaacgtgc tttacggacc cgatgctcct 720
178 acaatcagcc ctctaaacac aagctataga tcaggggaaa atctgaatct gagctgtcat 780
179 gccgctagca atcctcccg ccaatacagc tggtttgtca atggcacttt ccaacagtcc 840
180 acccaggaac tgttcattcc caatattacc gtgaacaata gtggatccta cacgtgccaa 900
181 gctcacaata gcgacaccgg actcaaccgc acaaccgtga cgacgattac cgtgtatgag 960
182 ccacaaaaac cattcataac tagtaacaat tctaaccag ttgaggatga ggacgcagtt 1020
183 gcattaactt gtgagccaga gattcaaaat accacttatt tatggtgggt caataaccaa 1080
184 agtttgccgg ttagcccacg cttgcagttg tctaatagata accgcacatt gacactcctg 1140
185 tccgttactc gcaatgatgt aggaccttat gagtgtggca ttcagaatga attatccgtt 1200
186 gatcactccg accctgttat ccttaatgtt ttgtatggcc cagacgaccc aactatatct 1260
187 ccatacata cctactaccg tcccggcgtg aacttgagcc tttcttgcca tgcagcatcc 1320
188 aacccccctg cacagtactc ctggctgatt gatggaaaca ttcagcagca tactcaagag 1380
189 ttatttataa gcaacataac tgagaagaac agcggactct atacttgcca ggccaataac 1440

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190 tcagccagtg gtcacagcag gactacagtt aaaacaataa ctgtttccgc ggagctgccc 1500
191 aagccctcca tctccagcaa caactccaaa cccgtggagg acaaggatgc tgtggccttc 1560
192 acctgtgaac ctgaggctca gaacacaacc tacctgtggt gggtaaattg tcaagacctc 1620
193 ccagtcagtc ccaggctgca gctgtccaat ggcaacagga ccctcactct attcaatgtc 1680
194 acaagaaatg acgcaagagc ctatgtatgt ggaatccaga actcagttag tgcaaaccgc 1740
195 agtgacccag tcaccctgga tgtcctctat gggccggaca ccccatcat ttcccccca 1800
196 gactcgtctt acctttcggg agcggacctc aacctctcct gccactcggc ctctaaccga 1860
197 tccccgcagt attcttggg tatcaatggg ataccgcagc aacacacaca agttctcttt 1920
198 atcgccaaaa tcacgcaaaa taataacggg acctatgcct gttttgtctc taacttgggt 1980
199 actggccgca ataattccat agtcaagagc atcacagtct ctgcatctgg aacttctcct 2040
200 ggtctctcag ctggggccac tgtcggcatc atgattggag tgctggttgg gggtgctctg 2100
201 atatag 2106
204 <210> SEQ ID NO: 4
205 <211> LENGTH: 371
206 <212> TYPE: PRT
207 <213> ORGANISM: Homo sapiens
209 <400> SEQUENCE: 4
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211 1 5 10 15
213 Pro Glu Ile Gln Asn Thr Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser
214 20 25 30
216 Leu Pro Val Ser Pro Arg Leu Gln Leu Ser Asn Asp Asn Arg Thr Leu
217 35 40 45
219 Thr Leu Leu Ser Val Thr Arg Asn Asp Val Gly Pro Tyr Glu Cys Gly
220 50 55 60
222 Ile Gln Asn Glu Leu Ser Val Asp His Ser Asp Pro Val Ile Leu Asn
223 65 70 75 80
225 Val Leu Tyr Gly Pro Asp Asp Pro Thr Ile Ser Pro Ser Tyr Thr Tyr
226 85 90 95
228 Tyr Arg Pro Gly Val Asn Leu Ser Leu Ser Cys His Ala Ala Ser Asn
229 100 105 110
231 Pro Pro Ala Gln Tyr Ser Trp Leu Ile Asp Gly Asn Ile Gln Gln His
232 115 120 125
234 Thr Gln Glu Leu Phe Ile Ser Asn Ile Thr Glu Lys Asn Ser Gly Leu
235 130 135 140
237 Tyr Thr Cys Gln Ala Asn Asn Ser Ala Ser Gly His Ser Arg Thr Thr
238 145 150 155 160
240 Val Lys Thr Ile Thr Val Ser Ala Glu Leu Pro Lys Pro Ser Ile Ser
241 165 170 175
243 Ser Asn Asn Ser Lys Pro Val Glu Asp Lys Asp Ala Val Ala Phe Thr
244 180 185 190
246 Cys Glu Pro Glu Ala Gln Asn Thr Thr Tyr Leu Trp Trp Val Asn Gly
247 195 200 205
249 Gln Ser Leu Pro Val Ser Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg
250 210 215 220
252 Thr Leu Thr Leu Phe Asn Val Thr Arg Asn Asp Ala Arg Ala Tyr Val
253 225 230 235 240
255 Cys Gly Ile Gln Asn Ser Val Ser Ala Asn Arg Ser Asp Pro Val Thr
256 245 250 255

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258 Leu Asp Val Leu Tyr Gly Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp
259           260           265           270
261 Ser Ser Tyr Leu Ser Gly Ala Asp Leu Asn Leu Ser Cys His Ser Ala
262           275           280           285
264 Ser Asn Pro Ser Pro Gln Tyr Ser Trp Arg Ile Asn Gly Ile Pro Gln
265           290           295           300
267 Gln His Thr Gln Val Leu Phe Ile Ala Lys Ile Thr Pro Asn Asn Gly
268 305           310           315           320
270 Thr Tyr Ala Cys Phe Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser
271           325           330           335
273 Ile Val Lys Ser Ile Thr Val Ser Ala Ser Gly Thr Ser Pro Gly Leu
274           340           345           350
276 Ser Ala Gly Ala Thr Val Gly Ile Met Ile Gly Val Leu Val Gly Val
277           355           360           365
279 Ala Leu Ile
280           370
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284 <211> LENGTH: 31
285 <212> TYPE: DNA
286 <213> ORGANISM: Artificial Sequence
288 <220> FEATURE:
289 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
290     primer
292 <400> SEQUENCE: 5
293 ggtaccggta ccatggaagg ggaaggggtt c                               31
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297 <211> LENGTH: 31
298 <212> TYPE: DNA
299 <213> ORGANISM: Artificial Sequence
301 <220> FEATURE:
302 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
303     primer
305 <400> SEQUENCE: 6
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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/579,025

DATE: 05/23/2006

TIME: 14:04:51

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L:10 M:270 C: Current Application Number differs, Replaced Current Application Number

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date